

The scores below are sorted by initial score. Significance is calculated based on initial scores.

אדרת הרים ותיכונם במקרא

100% identical sequence to

> O <
 O 10 IntelliGenetics
 > O <
 FastDB - Fast Pairwise Comparison of Sequences
 Release 5.4

Results file seq71-q9sjq6.res made by bobryen on Tue 17 Dec 102 12:54:30-PST.

Query sequence being compared: SEQ71-Q9SJQ6 (1-90)
 Number of sequences searched: 4
 Number of scores above cutoff: 4

Results of the initial comparison of SEQ71-Q9SJQ6 (1-90) with:
 File : seq71compares.pep

Residue	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40		
N	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
U	50	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
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SCORE	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-				
STDEV	8	-7	-7	-6	-6	-5	-5	-4	-4	-3	-3	-2	-2	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1							

Similarity matrix PAM-150 K-tuple 1
 Threshold level of sim. 16%
 Mismatch penalty 1 Joining penalty 1
 Gap penalty 5.00 Window size 90
 Gap size penalty 0.05
 Cutoff score 0.1
 Randomization group 0

PARAMETERS

SEARCH STATISTICS

Score	Mean	Median	Standard Deviation
Times:	00:00:00.00	00:00:00.00	00:00:00.00
Number of residues:	4350	-	-
Number of sequences searched:	4	-	-
Number of scores above cutoff:	4	-	-

The scores below are sorted by initial score.
 Significance is calculated based on initial score.
 A 100% identical sequence to the query sequence was not found.

The list of best scores is:

PARAMETERS			
Similarity matrix	PAM150	K-tuple	1
Threshold level of sim.	16%		
Mismatch penalty	1	Joining penalty	20
Gap penalty	5.00	Window size	208
Gap size penalty	0.05		
Cutoff, score	1		
Database, accession	2		

SEARCH STATISTICS	
Scores:	Mean 92
Times:	Median 58
	Standard Deviation 35.00
	Total Elapsed 00:00:00
	CPU 00:00:00

Number of residues:	3817
Number of sequences searched:	5
Number of scores above cutoff:	5

The scores below are sorted by initial score. Significance is calculated based on initial score.

The list of best scores is:

PARAMETERS			
Similarity matrix	PAM-150	K-tuple	1
Threshold level of sim.	16%		
Mismatch Penalty	1	Joining Penalty	20
Gap Penalty	1.00	Window size	88
Gap size Penalty	0.05		
Cutoff score	1		

10

SEARCH STATISTICS			
Scores :	Mean	Median	Standard Deviation
Times :	58	55	6.08
CPU	22	20	Total Elapsed

00:00:00.00

re.

3

was not found

The scores below are sorted by initial score. Significance is calculated based on initial score.

- 1 -

A 100% identical sequence to the query sequence was

80 PDXAKXXLISXGIGLKSVECVRLXIXXAFPVDTN 90 SVECVRLXIXXAFPVDTN 100 GRIAVRLGVNPLOPLPXXQXHX
110 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
120 X 130
PDKAKEYLLSIRGLKSVECVRLTLLHAFPVDTN 90 GRIAVRLGVNPLOPLPXXQXHX
80 90 100 110 X
